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$$\begin{aligned} \text{Proof.} \quad & \text{Let } \mathcal{A} = \{A_1, \dots, A_n\} \text{ be a family of } n \text{ sets.} \\ & \text{Define } \mathcal{B} = \{B_1, \dots, B_n\} \text{ where } B_i = A_i \cup \{x_i\} \text{ and } x_i \notin A_i. \\ & \text{Then } \mathcal{B} \text{ is a family of } n \text{ sets, and } \mathcal{A} \subseteq \mathcal{B}. \\ & \text{Since } x_i \notin A_i, \text{ we have } A_i \subsetneq B_i \text{ for all } i. \\ & \text{Therefore, } \mathcal{A} \text{ is a proper subset of } \mathcal{B}. \quad \square \end{aligned}$$

Received: November 12, 2002; accepted: March 4, 2003

212.4⁵ Million of 444,000,000
$$U^2 = (U_1 - X_1)(U_1 - U_2) = 7 - 2X_1$$

THE UNIVERSITY OF CHICAGO

$$\|f\|_{M(\mu)} = \inf_{F \in \mathcal{F}} \|F\|_{M(\mu)},$$

Submitted: 92612 steps, 14418503 residues

total number of hits satisfying chosen parameters: 426,124

Maximal length: 20000

[illegible]

Listing 45 Summary

index

Published_Applications_AA: *

[illegible]

Foot. No. is the number of results protected by chance to have a score greater than or equal to the score of the result being protected and is derived by analysts of the total score distribution.

SUMMARY

Row	Serial No.	Score	Score	Match	Length	LB	LB	Insert	Ref. Code
1	864	100.0	1.5	10	05-09-864-917.2	Sequence 2, Appl		Sequence 2, Appl	
2	844	49.9	1.5	10	05-09-869-917.4	Sequence 1, Appl		Sequence 1, Appl	
3	94	10.9	6.0	10	05-09-864-917.17	Sequence 1, Appl		Sequence 1, Appl	
4	75	8.7	5.24	10	05-09-925-908.15.68	Sequence 1, Appl		Sequence 1, Appl	
5	91	6.2	6.9	10	05-09-925-908.15.68	Sequence 1, Appl		Sequence 1, Appl	
6	71	8.2	6.68	10	05-09-801-868.2.48	Sequence 2, Appl		Sequence 2, Appl	
7	80	8.0	7.08	10	05-09-945-258.1.19	Sequence 1, Appl		Sequence 1, Appl	
8	69	8.0	10.12	10	05-09-285-486.0.14	Sequence 4, Appl		Sequence 4, Appl	
9	68	7.9	25.3	10	05-09-815-242.1.68.6	Sequence 1, Appl		Sequence 1, Appl	
10	67.5	7.8	41.7	10	05-09-806-055.11.9	Sequence 1, Appl		Sequence 1, Appl	
11	66	7.7	15.9	10	05-09-864-761.4.5.91	Sequence 1, Appl		Sequence 1, Appl	
12	66	7.7	4.91	10	05-09-881-752.6.1.28	Sequence 1, Appl		Sequence 1, Appl	
13	66	7.7	7.09	15	05-09-945-258.1.14	Sequence 2, Appl		Sequence 2, Appl	
14	66	7.7	8.07	10	05-09-847-868.6.2	Sequence 2, Appl		Sequence 2, Appl	
15	66	7.6	21.57	10	05-09-861-868.6.2	Sequence 5, Appl		Sequence 5, Appl	
16	65.5	7.5	25.0	10	05-09-845-242.1.6.15	Sequence 1, Appl		Sequence 1, Appl	
17	65.5	7.5	41.3	10	05-09-866-055.5.9.9	Sequence 1, Appl		Sequence 1, Appl	
18	65	7.5	1.55	10	05-09-785-770.8.1.2	Sequence 1, Appl		Sequence 1, Appl	
19	65	7.5	1.25	10	05-09-785-770.8.1.9	Sequence 1, Appl		Sequence 1, Appl	

20	65	7.5	7.6	10	OS-09-864.7-76.4-1.1	Sequencer 24.0	AT
21	65	7.5	186	10	OS-09-764.84-76.4-1	Sequencer 24.0	AT
22	65	7.5	410	10	OS-09-785.77-78.6-1	Sequencer 24.0	AT
23	65	7.5	1907	10	OS-09-785.77-78.6-1	Sequencer 24.0	AT
24	65	7.5	2489	10	OS-09-95.1-84.2-5	Sequencer 24.0	AT
25	64.5	7.5	511	10	OS-09-823.9-98.6-6	Sequencer 24.0	AT
26	64	7.4	646	10	OS-09-841.1-132.5-7	Sequencer 24.0	AT
27	64	7.4	655	10	OS-09-845.5-85-2	Sequencer 24.0	AT
28	63.5	7.4	237	10	OS-09-815.2-42.1-3	Sequencer 24.0	AT
29	63.5	7.4	429	10	OS-09-815.2-42.1-3	Sequencer 24.0	AT
30	63.5	7.4	723	10	OS-09-815.2-42.1-3	Sequencer 24.0	AT
31	62.5	7.4	263	10	OS-09-925.3-100-1-2	Sequencer 24.0	AT
32	63	7.3	263	10	OS-09-925.3-100-1-2	Sequencer 24.0	AT
33	63	7.3	302	10	OS-09-815.2-42.1-3	Sequencer 24.0	AT
34	63	7.3	897	10	OS-09-815.2-42.1-3	Sequencer 24.0	AT
35	62.5	7.3	236	10	OS-09-803.2-88.6-5	Sequencer 24.0	AT
36	62.5	7.3	5703	10	OS-09-864.7-76.4-1	Sequencer 24.0	AT
37	62	7.2	140	10	OS-09-952.7-70.2-2	Sequencer 24.0	AT
38	61.5	7.1	147	10	OS-09-729.6-74-2	Sequencer 24.0	AT
39	61.5	7.1	262	10	OS-09-815.2-42.1-3	Sequencer 24.0	AT
40	61	7.1	140	10	OS-09-815.2-42.1-3	Sequencer 24.0	AT
41	61	7.1	212	10	OS-09-934.9-101-3	Sequencer 24.0	AT
42	61	7.1	212	10	OS-09-934.9-101-3	Sequencer 24.0	AT
43	61	7.1	862	10	OS-09-794.5-54-2	Sequencer 24.0	AT
44	61	7.1	868	10	OS-09-845.5-85-2	Sequencer 24.0	AT
45	61	7.1	261	10	OS-09-841.1-132.5-7	Sequencer 24.0	AT

ALIGNMENT

RESULT 1

THE UNIVERSITY OF CHICAGO

MILLER, CLARA, HULLIK S.
; RUBEN, STEVEN M.

NUMBER OF STUDENTS: 17
CURRENT HOME ADDRESS:
STREET ADDRESS:
CITY:

	006	007	008	009	010	011	012	013	014	015	016	017	018	019	020	021	022	023	024	025	026	027	028	029	030	031	032	033	034	035	036	037	038	039	040	041	042	043	044	045	046	047	048	049	050	051	052	053	054	055	056	057	058	059	060	061	062	063	064	065	066	067	068	069	070	071	072	073	074	075	076	077	078	079	080	081	082	083	084	085	086	087	088	089	090	091	092	093	094	095	096	097	098	099	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515
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STATE: IL
COUNTY: ILSA

MECHANISM TYPE: PLATE AND RISK

CHERATIN; SYSLIM, 10⁻⁴(10/5/MS)-005

CURRENT APPLICATION DATA
 ATTACHED AT BOTTOM OF PAGE

CLASSIFICATION: Unknown
 PROBABILE APPROPRIATION: 100%

PLANNING DATE: UNKNOWN

FILED DATE: 07-11-1997
ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 6,688
 IDENTIFICATION NUMBER: 138 0440002

TELEPHONE: 202-471-2600
TELETYPE: 202-471-4444

SINGH, CHAKRABORTY

TYPE: amino acid
TOPLOGY: linear

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1 MOLECULE TYPE: protein
2 SPECIFIC CHARACTERISTICS: seq. no. 105-09-017-2
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[illegible]

Search completed: November 12, 2002, 09:26:49
Jedi Time : 12 Steps

Copyright (c) 1994 - 2002 Computer 130.

MM Protein Protein search, using sw model

Run on: November 12, 2002, 09:26:56 / Search Time: 17 Seconds

(without alignments) 916.104 Million cell updates/sec

Title: US-09-899-917-2

Protein Score: 162

Sequence: 1 MPEPTALELWETTFEPTV.....EATIKESVAVANATIRIS 172

Search Length: 61100

Gap: 60.0 / Gap: 60.0

Word Size: 16

Total number of hits satisfying chosen parameters: 0

Minimum hit seq length: 0

Maximum hit seq length: 200000000

Post processing: listing first 1000 summaries

Database: p1k_73:*

1: p11:*

2: p12:*

3: p13:*

4: p14:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Prod. No.	Score	Match	Length	DB	ID	Description
No matches found						

Search completed: November 12, 2002, 09:29:12

Job time: 17 secs

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GenBank Version 5.1.4
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FASTA format protein search, using SW model

Run on: November 12, 2002, 09:23:55 : Search time 1.2 seconds

(without alignment)
559,940 Million cell updates/sec

Title: US-09-899-917-2

Perfect score: 162

Sequence: 1 MCDTALPHEWLLPNSNR.....ELTEKSTVAVANALIMRS 162

Scoring table: cellpro

Gapop 60.00 / Gapext 60.00

Search: 112892 seqs, 4147028 residues

Word size: 16

Total number of hits satisfying chosen parameters: 2

Minimum db seq length: 5

Maximum db seq length: 20000000

Post-processing: listing first 1000 similarities

Database: 1 SwissProt.401*

Prod. No. is the number of results produced by choice to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY

Result	No.	Score	Matrix	Length	db	ID	Description
1	162	100.0	162	1	MD1_HUMAN	094711	human surface
2	23	14.2	162	1	MD1_MOUSE	094711	mouse

ALIGNMENTS

MD1_HUMAN STANDARD; PRT; 162 AA.

MD1_MOUSE STANDARD; PRT; 162 AA.

MD1_MOUSE STANDARD; PRT; 162 AA.

MD1_MOUSE STANDARD; PRT; 162 AA.

MD1_MOUSE STANDARD; PRT; 162 AA.

MD1_MOUSE STANDARD; PRT; 162 AA.

MD1_MOUSE STANDARD; PRT; 162 AA.

MD1_MOUSE STANDARD; PRT; 162 AA.

MD1_MOUSE STANDARD; PRT; 162 AA.

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MD1_MOUSE STANDARD; PRT; 162 AA.

MD1_MOUSE STANDARD; PRT; 162 AA.

Genome version 5.1.1
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QM Protein - Protein search, using sw model

Run on: November 12, 2002, 09:26:26 : Search time 41 seconds

(without alignments)
1076,762 Million cell operators/sec

File: us-09-899-917-2

Protein source: 1 MESTAT1E.WILLIAMS2002.....EVIDENCE/ANNOTATIONS 19.2

Sequence:

Scanned from: 0110
Gap: 60.0 : Gap: 60.0

Search: 67156 seqs, 2004715 residues

Word size: 10

Total number of hits satisfying chosen parameters: 0

Minimum for seq length: 0

Maximum for seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database:

SIKREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_humans:*
5: sp_invertebrates:*
6: sp_mammals:*
7: sp_mice:*
8: sp_organisms:*
9: sp_phages:*
10: sp_plants:*
11: sp_rodents:*
12: sp_viruses:*
13: sp_vertebrates:*
14: sp_unclassified:*
15: sp_viruses:*
16: sp_bacteriophage:*
17: sp_archaea:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY

Prod. No.	Score	Match length (8-10)	Prod. No.
No matches found			

Search completed: November 12, 2002, 09:28:27
Job time: 41 secs





GenCorp Version 5.1.4
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com protein - protein search, using SW model

Run on: November 12, 2002, 09:26:41 Search time: 15 seconds
(without alignments)
417.768 Million cell updates/sec

Title: US-09-899-917-2

Perfect score: 162

Sequence: 1 P2MTAIIPLMTIITSTGSI

PIPERIDINE ANALYSES 162

Scoring table:

Gapop 60.0, Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size: 10

Total number of hits satisfied chosen parameters: 1

Minimum DB seq length: 6

Maximum DB seq length: 200000000

Post-processing: listing first 1000 summaries

Database: 1 Issued_Patents_AA*

1: 162 162 162 162 162 162 162 162 162 162
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prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Match	Length	DB	ID	Score	Prod. No.
1	162	160.0	162	4	US-08-994-962-2	Sequence 2, Appx 3	

ALIGNMENTS

RESULT 1
US-08-994-962-2
Sequence 2 Affiliation: US/09991962
Patent No. 6281486
GENERAL INFORMATION:
APPLICANT: OLSEN, Henrik S.
APPLICANT: RUBEN, Steven M.
TITLE OF INVENTION: Human Inocence Induced Secreted protein
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESS: Steven, Kossler Goldstein & Fox P.C.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
SOFTWARE: IBM PC compatible
OPERATING SYSTEM: PC C/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.0

CURRENT APPLICATION DATA:
1 APPLICATION NUMBER: 09/07994, 962
2 FILING DATE: notwith
3 CLASSIFICATION:
4 PRIOR APPLICATION DATA:
5 APPLICATION NUMBER: US 62/703,869
6 FILING DATE: 20 DEC-1996
7 CLASSIFICATION:
8 PRIOR APPLICATION DATA:
9 APPLICATION NUMBER: 09/07994, 962
10 FILING DATE: 07-FEB-1997
11 CLASSIFICATION:
12 ALTERNATE/ABBREV. NAME:
13 NAME: Steven, Kossler Goldstein & Fox P.C.L.L.C.
14 REFERENCE NUMBER: 162, 162
15 TELEPHONE: 202 471-2600
16 TELEFAX: 202 471-2600
17 INFORMATION FOR SEQ ID NO: 4:
18 SEQUENCE CHARACTERISTICS:
19 LENGTH: 162 amino acids
20 TYPE: amino acid
21 TOPOLOGY: linear
22 MOLECULE TYPE: protein
23 US-08-994-962-2

Query Match: 160.0% Score: 162 DB: 4 Length: 162
Best Local Similarity: 100.0% Prod. No.: 6,961,542
Matches: 162, Gaps: 0, Mismatches: 0, Indels: 0, Inps: 0
1: 162 162 162 162 162 162 162 162 162 162
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PR	23-APR-1999	9908-0140891	PR	20-JUL-1999	9908-0144444
PR	23-APR-1999	9908-0141449	PR	21-JUL-1999	9908-0144444
PR	40-APR-1999	9908-0142048	PR	21-JUL-1999	9908-0144444
PR	51-APR-1999	9908-0142467	PR	21-JUL-1999	9908-0144444
PR	04-MAY-1999	9908-0142484	PR	21-JUL-1999	9908-0144444
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PR	11-MAY-1999	9908-0144248	PR	23-JUL-1999	9908-0144444
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PR	14-MAY-1999	9908-0144340	PR	27-JUL-1999	9908-0144444
PR	14-MAY-1999	9908-0144341	PR	27-JUL-1999	9908-0144444
PR	21-MAY-1999	9908-0145124	PR	27-JUL-1999	9908-0144444
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PR	25-MAY-1999	9908-0145629	PR	02-AUG-1999	9908-0144444
PR	25-MAY-1999	9908-0146021	PR	02-AUG-1999	9908-0144444
PR	27-MAY-1999	9908-0146342	PR	03-AUG-1999	9908-0144444
PR	27-MAY-1999	9908-0146342	PR	04-AUG-1999	9908-0144444
PR	01-JUN-1999	9908-0147242	PR	05-AUG-1999	9908-0144444
PR	01-JUN-1999	9908-0147242	PR	05-AUG-1999	9908-0144444
PR	04-JUN-1999	9908-0147526	PR	05-AUG-1999	9908-0144444
PR	07-JUN-1999	9908-0147724	PR	06-AUG-1999	9908-0144444
PR	08-JUN-1999	9908-0148044	PR	06-AUG-1999	9908-0144444
PR	11-JUN-1999	9908-0148340	PR	09-AUG-1999	9908-0144444
PR	11-JUN-1999	9908-0148340	PR	10-AUG-1999	9908-0144444
PR	14-JUN-1999	9908-0149442	PR	11-AUG-1999	9908-0144444
PR	14-JUN-1999	9908-0149442	PR	12-AUG-1999	9908-0144444
PR	18-JUN-1999	9908-0149444	PR	13-AUG-1999	9908-0144444
PR	18-JUN-1999	9908-0149445	PR	13-AUG-1999	9908-0144444
PR	18-JUN-1999	9908-0149445	PR	17-AUG-1999	9908-0144444
PR	18-JUN-1999	9908-0149447	PR	18-AUG-1999	9908-0144444
PR	18-JUN-1999	9908-0149449	PR	20-AUG-1999	9908-0144444
PR	18-JUN-1999	9908-0149449	PR	20-AUG-1999	9908-0144444
PR	18-JUN-1999	9908-0149449	PR	23-AUG-1999	9908-0144444
PR	18-JUN-1999	9908-0149449	PR	23-AUG-1999	9908-0144444
PR	18-JUN-1999	9908-0149449	PR	25-AUG-1999	9908-0144444
PR	18-JUN-1999	9908-0149449	PR	25-AUG-1999	9908-0144444
PR	21-JUN-1999	9908-0149449	PR	27-AUG-1999	9908-0144444
PR	22-JUN-1999	9908-0149449	PR	27-AUG-1999	9908-0144444
PR	23-JUN-1999	9908-0149449	PR	30-AUG-1999	9908-0144444
PR	24-JUN-1999	9908-0149449	PR	31-AUG-1999	9908-0144444
PR	24-JUN-1999	9908-0149449	PR	07-SEP-1999	9908-0152464
PR	28-JUN-1999	9908-0149449	PR	10-SEP-1999	9908-0153070
PR	30-JUN-1999	9908-0149449	PR	13-SEP-1999	9908-0153758
PR	01-JUL-1999	9908-0149449	PR	15-SEP-1999	9908-0154018
PR	01-JUL-1999	9908-0149449	PR	16-SEP-1999	9908-0154018
PR	02-JUL-1999	9908-0149449	PR	20-SEP-1999	9908-0154018
PR	06-JUL-1999	9908-0149449	PR	22-SEP-1999	9908-0154018
PR	06-JUL-1999	9908-0149449	PR	22-SEP-1999	9908-0154018
PR	09-JUL-1999	9908-0149449	PR	24-SEP-1999	9908-0154018
PR	12-JUL-1999	9908-0149449	PR	24-SEP-1999	9908-0154018
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PR	13-JUL-1999	9908-0149449	PR	28-SEP-1999	9908-0154018
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PR	15-JUL-1999	9908-0149449	PR	04-OCT-1999	9908-0152717
PR	16-JUL-1999	9908-0144005	PR	05-OCT-1999	9908-0152717
PR	16-JUL-1999	9908-0144005	PR	06-OCT-1999	9908-0152717
PR	16-JUL-1999	9908-0144005	PR	07-OCT-1999	9908-0152717
PR	19-JUL-1999	9908-0144444	PR	08-OCT-1999	9908-0152717
PR	19-JUL-1999	9908-0144444	PR	12-OCT-1999	9908-0152717
PR	19-JUL-1999	9908-0144444	PR	13-OCT-1999	9908-0152717
PR	19-JUL-1999	9908-0144444	PR	13-OCT-1999	9908-0152717

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F16	21.00E1-19999	9901S-0160770
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F16	21.00E1-19999	9901S-0160815
F16	22.00E1-19999	9901S-0160980
F16	22.00E1-19999	9901S-0160981.1
F16	22.00E1-19999	9901S-0160989.9
F16	25.00E1-19999	9901S-0161404
F16	25.00E1-19999	9901S-0161405
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F16	26.00E1-19999	9901S-0161493
F16	29.00E1-19999	9901S-0162142

Unit 7 Math

Source 77:

$$I_1 = \int_{\mathbb{R}^n} |f(x)|^p dx$$

Best local similarity	24.08	Prod. No.	4.6
Matches	17	Mismatches	40
		Gaps	4

Matches 2

iv. 17; Mishnah (1:1)

40; Models 42; Caps

4

48 COLLEGE PARK, MARYLAND
U.S. GOVERNMENT PRINTING OFFICE 1964

204 VORONOV, G. I. *POI NÁVŠTĚVY VĚSTNÍK* A 29

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2,2

105 ALBERT, GORDON, YVONNE, and J. POLYMER LETTERS, 1, 147

1999 ALFAKMI,HEL.MOYDVAVAT'PEPEYEL --- FULMNNIYILK 348

Submitted: 12/2/2019; Accepted: 12/2/2019; Published: 12/2/2019

Journal of Management Education

Page 10

Great Mallard 100.0%; Sexes 95.2; DB 4; Length 16.2
Best local similarity 100.0%; Pred. No. 4.3e-100;


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1 Patent No. 24064
2
3 GENERAL INFORMATION:
4 APPLICANT: Ratti, Giulio
5 APPLICANT: Comandotti, Maurizio
6 APPLICANT: Poggio, Mario F.
7 APPLICANT: Giuliano, Maurizio M.
8 TITLE OF INVENTION: FISH FLAVORED ISOLATE FROM CHLAMYDIA
9 TITLE OF INVENTION: FISH FLAVORED FRYING OILS ARE PREPARED BY
10 TITLE OF INVENTION: FISH FOR ORNAMENTAL FISHING FOR THE EXPRESSION OF SAID
11 TITLE OF INVENTION: GENES IN HERBICIDE SYSTEMS, PREPARATION OF SAID
12 NUMBER OF SEQUENCES: 24
13 ADDRESS OF INVENTOR:
14 Addressed: Danilo Clemente, Renato A. Faria
15 STREET: 401 N. Washington Street
16 CITY: Falls Church
17 STATE: Virginia
18 COUNTRY: USA
19 ZIP: 22046-0747
20 REGISTERED MAILABLE FORM:
21 MEDIUM TYPE: Floppy disk
22 COMPUTER: IBM PC compatible
23 OPERATING SYSTEM: PC-DOS/MS-DOS
24 SOFTWARE: Patent Release #1.0, Version #1.25
25
26 CURRENT APPLICATION DATA:
27 APPLICATION NUMBER: US/08/468,544
28 FILING DATE: 06-JUN-1995
29 CLASSIFICATION: A35
30 PRIOR APPLICATION DATA:
31 APPLICATION NUMBER: US 07/661,820
32 FILING DATE: 28-FEB-1991
33 APPLICATION NUMBER: 11 M 91A000414
34 FILING DATE: 07-FEB-1991
35 ALTERNATIVE/AGENT INFORMATION:
36 NAME: Svensson, Leonard R.
37 REGISTRATION NUMBER: 48,430
38 REGISTRATION FEE RECEIPT: 1267 202P
39 TELECOMMUNICATION INFORMATION:
40 TELEPHONE: 703-241-1400
41 TELEFAX: 703-241-2848
42
43 INDEX: 240645
44 INFORMATION FOR SEQ ID NO: 16:
45 SEQUENCE CHARACTERISTICS:
46 LENGTH: 294 amino acids
47 TYPE: amino acid
48 TOPLOGY: linear
49 MOLECULE TYPE: protein
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1 TITLE OF INVENTION: CANINE BEHAVIORAL DEFECT AND ADAPTATION DEFECTS
2 NUMBER OF SEQUENCE: 91
3 CORRESPONDENCE ADDRESS:
4 ADDRESS: GUTHRIE, MOLLIS & SATTORF
5 STREET: 530 Fifth Avenue
6 CITY: New York
7 STATE: NY
8 COUNTRY: USA
9 ZIP: 10036
10 COMPUTER READABLE FORM:
11 MEDIA TYPE: Floppy disk
12 OPERATOR: IBM PC compatible
13 SOFTWARE: Patent Defect Detector Version #1.25
14 CURRENT APPLICATION DATA:
15 APPLICATION REFERENCE: 07/007250, 151
16 FILING DATE: 30 MAR 1994
17 CLASSIFICATION: A65
18 ATTORNEY/AGENT INFORMATION:
19 NAME: Frommer, William S.
20 REGISTRATION NUMBER: 27,906
21 REFERENCE/CHECK NUMBER: 44-1-273
22 TELECOMMUNICATION INFORMATION:
23 TELEPHONE: (212) 640-3333
24 TELEFAX: (212) 640-0712
25 INDEX: 425066 CURTIS
26 INFORMATION FOR SEQ ID NO: 22:
27 SEQUENCE CHARACTERISTICS:
28 LENGTH: 442 amino acids
29 TYPE: amino acid
30 STRANDEDNESS: single
31 topology: linear
32 MODIFIABLE TYPE: polypeptide
33 FRAGMENT TYPE: N-terminal
34 DS-OR-220-151-22
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36 QUOTE MATCH R (%), Score 74.91, OR 1, Length 442
37 Post Local Similarity 25.4%, Pred. No. 1, 1:
38 Matches 4% Conserved 17% Missed 62% Indels 4% Gap 2%
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40 QY 2 KPEPLATWLTTPSSNSDSDTKAMTHVVSLSLVYSTLGLQDSNYSKSG...
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42 | 141 KYSAKL-TWRIMR13 -ATHH - - - - - IVSYRR-NIKSTAM14
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50 DB 279 -CTATLMISGDLRKILLYGRLEVTFPTLDRNITP-WDEMTWKW 37
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52
53 RESULT 8
54 DS-OR-118-118-22
55 Sequence 22 Application 07/007250, 118
56 Patent No. 5298920
57 GENERAL INFORMATION:
58 APPLICANT: PAOLETTI, ENZO
59 APPLICANT: LIMACH, KELIA L
60 TITLE OF INVENTION: NEURONAL ANTIMETASTATIC SEQUENCES OF
61 TITLE OF INVENTION: CANINE DEPRESSORS 49, 5, AND 4D AND OTHER EFFECT
62 NUMBER OF SEQUENCES: 159
63 CORRESPONDENCE ADDRESS:
64 ADDRESSEE: DUPUIS, ROBERT & SATOUD, P.O.
65 STREET: 540 FIFTH AVENUE, 25TH FLOOR
66 CITY: NEW YORK
67 STATE: NEW YORK
68 COUNTRY: UNITED STATES OF AMERICA
69 ZIP: 10036
70 COMPUTER READABLE FORM:
71 MEDIA TYPE: Floppy Disk
72 COMMENTS: IBM PC compatible

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APPLICATION NUMBER: 08/717,118
FILING DATE:
ATTORNEY/AGENT INFORMATION:

720 NUTRITION AND AGING

Database version 5.1.1
Compiled (c) 1998 - 2002 Compugen Ltd.

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	Prod. No.	Database
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Result ID	Score	Query	Match Length	Prod. No.	Database
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 99. \mathcal{H}
 100. \mathcal{H}

[illegible][illegible]

